SEQUENCE LISTING

<110> ZIMMET, PAUL Z.
COLLIER, GREGORY

<120> A NOVEL GENE AND USES THEREFOR

<130> 22975-20007.00

<140> 09/331,930
<141> 1999-06-30

<150> PCT/AU98/00902
<151> 1998-10-30

<150> AU PP0117/97
<151> 1997-10-31

<150> AU PP0323/97
<151> 1997-11-11

<160> 27

<170> PatentIn Ver. 2.1

<210> 1
<211> 342
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: DNA sequence for beacon from unknown organism

<220>
<221> CDS
<222> (29)..(247)

<400> 1

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gttccaggag attacagctc cagccaca atg att gag gtg gtt tgc aac gac    52
                                 Met Ile Glu Val Val Cys Asn Asp
                                   1               5

cgt cta gga aag aaa gtc cgc gtt aag tgc aac acc gat gac acc atc   100
Arg Leu Gly Lys Lys Val Arg Val Lys Cys Asn Thr Asp Asp Thr Ile
     10                  15                  20

ggg gac ttg aag aaa ctg ata gcg gcc caa act ggc act cgt tgg aat   148
Gly Asp Leu Lys Lys Leu Ile Ala Ala Gln Thr Gly Thr Arg Trp Asn
 25                  30                  35                  40

aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct   196
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
                45                  50                  55

ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac   244
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
            60                  65                  70
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cag tagaggggaa ttcctccacc ttgcccaacc ttgctttcct ctcccatggc 297
Gln

tcatttaaca ctgttgtaga tgctcatttt tttgttaagt gtact 342

<210> 2
<211> 73
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Amino acid sequence for beacon from unknown organism

<400> 2
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp
50 55 60

Gly Met Asn Leu Glu Leu Tyr Tyr Gln
65 70

<210> 3
<211> 391
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Complimentary sequence for SEQ ID NO: 1

<400> 3
atgttcaaca cagcagccat ccaaggtcct ctaatgtcga ggtcggtgtt actaactcca 60
ccaaacgttg ctggcagatc ctttctttca ggcgcaattc acgttgtggc tactgtggta 120
gcccctgaac ttctttgact atcgccgggt ttgaccgtga gcaaccttat tctagcaaga 180
atttttcacc atgtgctaaa aattcctggt acatagagac cctctaatac tttaggtgct 240
accctacttg gacctcgaaa taatggtcat ctccccttaa ggaggtggaa cgggttggaa 300
cgaaaggaga gggtaccgag taaattgtga caacatctac gagtaaaaaa acaattcaca 360
tgaataaaaa ctttgatgct gcaaaaaaaa a 391

<210> 4
<211> 16
<212> DNA
<213> Artificial Sequence

52

A

<220>
<223> Description of Artificial Sequence: Primer

<400> 4
aagctttttt tttttg 16

<210> 5
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
aagcttcggg taa 13

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
agtccgcgtt aagtgcaaca 20

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
ctccaggttc atcccatcgt 20

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggctacagct tcaccaccac 20

<210> 9
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gcttgctgat ccacatctgc 20

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 10
tggtaataaa gctccaggtt catcccatcg 30

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
caaactggca ctcgttggaa 20

<210> 12
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
gttgggcaag gtggaggaa 19

<210> 13
<211> 102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(99)

<220>
<221> modified_base
<222> (44)
<223> a, t, c or g

<400> 13
atg atc gag gtt gtt tgc aac gac cgt ctg ggg aaa aag gtc cnc gtt 48
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Xaa Val
1 5 10 15

aaa tgc aac acg gat gat acc atc ggg gac ctt aag aag ctg att gca 96
Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

gcc taa 102
Ala

<210> 14
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (15)
<223> variable amino acid

<400> 14
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Xaa Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala

<210> 15
<211> 222
<212> DNA
<213> Psammomys obesus

<220>
<221> CDS
<222> (1)..(99)

<400> 15
aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct 48
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15

ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac 96
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

cag tagaggggaa ttcctccacc ttgcccaacc ttgctttcct ctcccatggc 149
Gln

tcatttaaca ctgttgtaga tgctcatttt taacaattca catgaataaa aactttgatg 209

55

A

ctgcaaaaaa aaa 222

<210> 16
<211> 33
<212> PRT
<213> Psammomys obesus

<400> 16
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15

Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

Gln

<210> 17
<211> 222
<212> DNA
<213> Psammomys obesus

<220>
<221> CDS
<222> (1)..(99)

<400> 17
aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct 48
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15

ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac 96
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

cag tagaggggaa ttcctccacc ttgcccaacc ttgctttcct ctcccatggc 149
Gln

tcatttaaca ctgttgtaga tgctcatttt taacaattca catgaataaa aactttgatg 209

ctgcaaaaaa aaa 222

<210> 18
<211> 33
<212> PRT
<213> Psammomys obesus

<400> 18
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15

Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

Gln

<210> 19
<211> 73
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Amino acid sequence for beacon from unknown organism

<400> 19
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp
50 55 60

Gly Met Asn Leu Glu Leu Tyr Tyr Gln
65 70

<210> 20
<211> 73
<212> PRT
<213> Homo sapiens

<400> 20
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp
50 55 60

Gly Met Asn Leu Glu Leu Tyr Tyr Gln
65 70

<210> 21
<211> 73
<212> PRT
<213> Murine sp.

A

<400> 21
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp
50 55 60

Gly Met Asn Leu Glu Leu Tyr Tyr Gln
65 70

<210> 22
<211> 73
<212> PRT
<213> Caenorhabditis elegans

<400> 22
Met Ile Glu Ile Thr Val Asn Asp Arg Leu Gly Lys Lys Val Arg Ile
1 5 10 15

Lys Cys Asn Pro Ser Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Glu Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Tyr Lys Asp His Ile Thr Leu Met Asp Tyr Glu Ile His Glu
50 55 60

Gly Phe Asn Phe Glu Leu Tyr Tyr Gln
65 70

<210> 23
<211> 66
<212> PRT
<213> Fasiola hepatica

<400> 23
Asp Arg Leu Gly Lys Lys Val Arg Val Lys Cys Asn Pro Thr Asp Lys
1 5 10 15

Val Gly Asp Leu Lys Lys Leu Ile Ala Ala Gln Thr Gly Thr Ala Pro
20 25 30

Glu Arg Ile Val Leu Lys Lys Trp Tyr Thr Ile Tyr Lys Asp His Val
35 40 45

Thr Leu Arg Asp Tyr Glu Ile Asn Asp Gly Met Asn Leu Glu Leu Tyr
50 55 60

A

Tyr Gln
65

<210> 24
<211> 73
<212> PRT
<213> Oryza sativa

<400> 24
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Tyr Lys Asp His Ile Thr Leu Ala Asp Tyr Glu Ile His Asp
50 55 60

Gly Met Gly Leu Glu Leu Tyr Tyr Asn
65 70

<210> 25
<211> 73
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Leu Lys Asp His Ile Cys Leu Glu Asp Tyr Glu Val His Asp
50 55 60

Gln Thr Asn Leu Glu Leu Tyr Tyr Leu
65 70

<210> 26
<211> 76
<212> PRT
<213> Homo sapiens

<400> 26
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

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Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
            20                  25                  30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
        35                  40                  45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
    50                  55                  60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
65                  70                  75
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<210> 27
<211> 60
<212> PRT
<213> Arabidopsis thaliana

<400> 27

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Gly Lys Thr Ile Ile Leu Glu Val Glu Ser Ser Asp Thr Ile Ala Asn
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Val Lys Glu Lys Ile Gln Val Lys Glu Gly Ile Lys Pro Asp Gln Gln
            20                  25                  30

Met Leu Ile Phe Phe Gly Gln Gln Leu Glu Asp Gly Val Thr Leu Gly
        35                  40                  45

Asp Tyr Asp Ile His Lys Lys Ser Thr Leu Tyr Leu
    50                  55                  60
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60

A